

logo

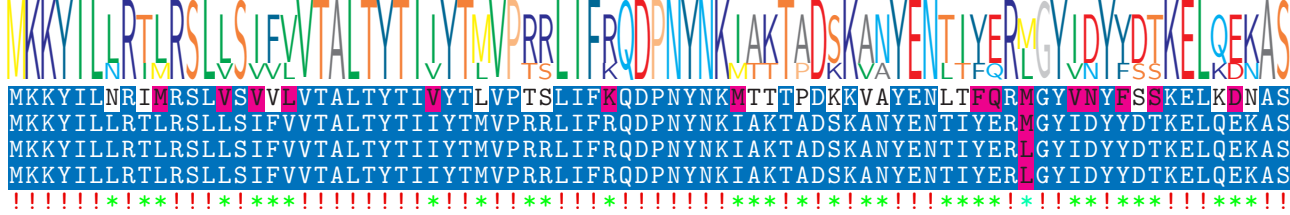
NTDB id 994633 AAFU62 RS01405 WP 002991105.1

NTDB id 476 HSISS4 RS06995 WP 013990225.1

NTDB id 293 STER RS06925 WP 011681416.1

NTDB id 325 STU RS16125 WP 002946410.1

consensus



Sequence logo for motif 1. The logo shows the conservation of amino acids across four sequences. The consensus sequence is indicated by the height of the letters. The motif is approximately 25 residues long, with a highly conserved region in the middle (residues 10-15) and more variable regions at the ends.

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logo

NTDB id 994633 AAFU62 RS01405 WP 002991105.1

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NTDB id 293 STER RS06925 WP 011681416.1

NTDB id 325 STU RS16125 WP 002946410.1

consensus



Sequence logo for motif 2. The logo shows the conservation of amino acids across four sequences. The consensus sequence is indicated by the height of the letters. The motif is approximately 25 residues long, with a highly conserved region in the middle (residues 10-15) and more variable regions at the ends.

160

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logo

NTDB id 994633 AAFU62 RS01405 WP 002991105.1

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NTDB id 293 STER RS06925 WP 011681416.1

NTDB id 325 STU RS16125 WP 002946410.1

consensus



Sequence logo for motif 3. The logo shows the conservation of amino acids across four sequences. The consensus sequence is indicated by the height of the letters. The motif is approximately 25 residues long, with a highly conserved region in the middle (residues 10-15) and more variable regions at the ends.

240

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logo

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NTDB id 325 STU RS16125 WP 002946410.1

consensus



Sequence logo for motif 4. The logo shows the conservation of amino acids across four sequences. The consensus sequence is indicated by the height of the letters. The motif is approximately 25 residues long, with a highly conserved region in the middle (residues 10-15) and more variable regions at the ends.

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logo

NTDB id 994633 AAFU62 RS01405 WP 002991105.1

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NTDB id 293 STER RS06925 WP 011681416.1

NTDB id 325 STU RS16125 WP 002946410.1

consensus



Sequence logo for motif 5. The logo shows the conservation of amino acids across four sequences. The consensus sequence is indicated by the height of the letters. The motif is approximately 25 residues long, with a highly conserved region in the middle (residues 10-15) and more variable regions at the ends.

400

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logo

NTDB id 994633 AAFU62 RS01405 WP 002991105.1

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NTDB id 293 STER RS06925 WP 011681416.1

NTDB id 325 STU RS16125 WP 002946410.1

consensus



Sequence logo for motif 6. The logo shows the conservation of amino acids across four sequences. The consensus sequence is indicated by the height of the letters. The motif is approximately 25 residues long, with a highly conserved region in the middle (residues 10-15) and more variable regions at the ends.

480

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478

478

logo

NTDB id 994633 AAFU62 RS01405 WP 002991105.1	DIVMTLVDPRIKLSTKKGK	500
NTDB id 476 HSISS4 RS06995 WP 013990225.1	DILMTVIDPRIKLTSKGGK.	497
NTDB id 293 STER RS06925 WP 011681416.1	DILMTIIDPRIKLTSKGGK.	497
NTDB id 325 STU RS16125 WP 002946410.1	DILMTIIDPRIKLTSKGGK.	497
consensus	!!*!!*!!!!!!**!*!*	

- non conserved
- similar
- ≥ 50% conserved